

Fig. 1A

G	S	V	A	C	P	P	P	A	Y	C	N	T	P	P	P	P	P	Y	E	166
GGG	AGT	GTG	GCC	TGC	CCG	CCC	CCT	CCA	GCC	TAC	TGC	AAC	ACG	CCT	CGG	CCC	CCG	TAC	GAA	632
Q	V	V	K	A	K	*														173
CAG	GTA	GTG	AAG	GCC	AAG	TAG														653

TGGGGTGCCACCGNGCAAGAGGGAGAGACAGGGAGGGCCTTTCCCTGGCCCTTCCTGTCCTCTGTTGATGTTCACTTCCAG
 GAACGGGTCICGTGGCCTGAAGGGCGTTCTGATACTTCCTGTCAGTCAGCAAGGAAAGCTCTTCCATGGTTTCATGG 732
 AGTACAATATAATGAACTCACACTTGTCTCTGTCACAGTCTGCTGTTCTGACGCTCTGTCAGGAGATCTACAGGAGAGA 811
 GGTGACAGTCCCCGAGGGTGAAGTCCTTAAGGTGGCTGAGCTGCTTACGGTGGGTGACAGATCTACAGGAGAGA 890
 TGGCTGGAGGTGCAAGTGGCATGTAGAGGGCAGGGCGAGATCCAGGGCAAGGATCCTCTGCCGGGATTAAATAGG 969
 AAGGCCCATGCCGGGGCTCAAGGCGATGAAGCCAGAGCGCAGACTGAGCTGAGGCCAGCAGGTCATCTGCCAGCCTG 1048
 CCTCTCTGTCAGCTCCCTTCAGAAGCTGTTGGAGAGACATTAGGGAGAGACCTGGCCAGGGCTGAGCTGAGGCCAG 1127
 CTGGTCATATCTAAAGATAGACTCTCTGACATGTCAGTGTACATCACAAGCAAAATTATTAAAGCTAGGGAAATCA 1206
 CTTAGAAATCAGGGCTTGGGGCTTGGGGCTGACATGTCAGTGTACATTCACAAGCAAAATTATTAAAGCTAGGGAAATCA 1285
 CTTGGCTGCCCAAACGTGAGACATTTGTCAGTGTACATTTGTCAGTGTACATTTGTCAGTGTACATTTGTCAGTGTAC 1364
 CTCTCCAGGGCATCTCAGGGCCGGGGTCTCCCTTAGGCAGCTCCAGGGGGCTGAGCTGAGCTGAGGCCAGGGCTGAGG 1443
 ACCTGGGGCACATCTGGCTGGGAAGTCAGATGGACTCTCAAGGGAGGGAGCTGAGGAGGGAGCTGAGCTGAGGCCAG 1522
 GTTGGGGTCAAGGGGTGTTGGCTGGGGCTCAAGGGAGGGAGCTGAGGAGGGAGCTGAGCTGAGGCCAGGGCTGAGG 1601
 TGGCACTGACCATGTTGTCATAAATGAGATAAAGAGAAGTGGCTGGGAATGAGATCTGGTGGZAAAGACAGGAGAA 1680
 CCCAGGGATUTCAGGTAGTCAGCTGCTGTTGAGTGTAGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1759
 TGTGTGAACGCTGACCTGTCTGCTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1838
 CACGGGGAAATGAGGTGGGGTGTCTTAAATGAGCTAAGGGAGATCTGGGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1917
 AGCATCAAGAACATCTCATGGAAAGTGGGATACGGGAGTGGGATCTGGTGGTCCATGCTTCACTGTTGAGCTGAGCTG 1996
 2075
 2154

Fig. 1B

Fig. 1C

Fig. 1D

C W Y F E G L Y P T Y I C R S Y E D C 45
 TGC TGG TAT TTT GAA GGA CTC TAT CCC ACA TAC TAT ATA TGC CGT TCC TAT GAA GAC TGC 271
 C G S R C C V R A L S I Q R L W Y F W F 65
 TGT GGC TCC AGG TGC TGT GTG AGG GCC CTT TCC ATA CAG AGG CTG TGG TAT TTT TGG TTC 331
 L L M M G V L F C C G A G F F I R R M 85
 CTG CTG ATG ATG GGT GTG CTG TTC TGC TGT GGT GCC GGT TTC TTC ATT CGC CGG CGC ATG 391
 Y P P L I E P T F N V S Y T R Q P P 105
 TAT CCG CCA CCA CTC ATT GAG GAG CCC ACA TTC AAT GTG TCC TAT ACC AGG CAG CCA CCA 451
 N P A P G A Q M G P P Y Y T D P G G P 125
 ATT CCT GCT CCA GGA GCA CAG CAA ATG GGA CCG CCA TAT TAC ACC GAC CCT GGA GGA CCC 511
 G M N P V G N T M A M A F Q V Q P N S P 145
 GGG ATG AAT CCT GTT GGC AAT ACC ATG GCT ATG GCT TTC CAG GTC CAG CCC AAT TCA CCT 571
 H G G T T Y P P P S Y C N T P P P Y 165
 CAC GGA GGC ACA ACT TAC CCA CCC CCT CCT TCC TAC TGC AAC ACG CCT CCA CCC CCC TAT 631
 E Q V V K D K * 173
 GAA CAG GTG GTG AAG GAC AAG TAG 655

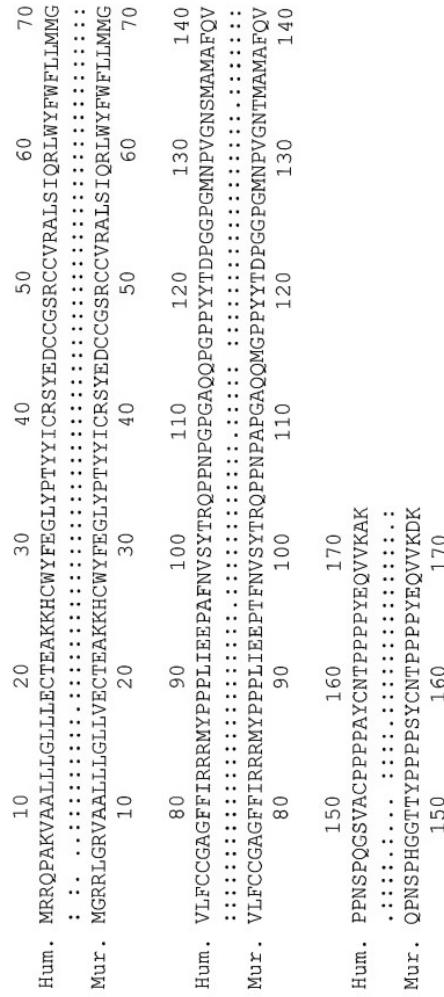
P.U.S.E.Y.T.L.D = T.T.C.T.T.G.G.T.T.A.C.C.T.C.A.C.C.G.A.T.A.C.T.G.C.T.G.A.T.G

Fig. 1E

CAAGATGCTCATCAAAGGCAAAAGGATGGACAGGGCCCTTTGGTTACCTTCCATCCGATACTTGCTGATAG 734

Fig. 1F

AGCTCTACTCTGTGCTGAGGTCCGTAGAGCGGGGTTGGCACAGACATAGGCAGACTTGTGCATGCTCTTC 2788
 TTGGCAACACTTGGCTCATATTCTCTGTTCTTGTATAAGTCTGTCTATGTTAAAAATAAAAGTG 2867
 AATTAGTCAAAAAAAGGGGGCGC 2915

Fig. 1G**Fig. 1H**

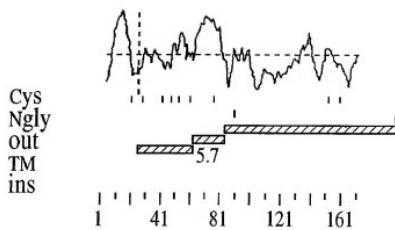


Fig. I

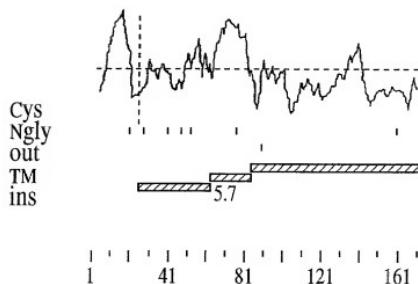


Fig. J

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Fig. 2A

		T T G C T T F G G - T T T S S S G G / G G																			
		I	F	K	G	L	L	N	R	N	L	Y	I	Q	Y	N	Q	V	S	F	
ATA	TTT	AAG	GGA	CTT	TTA	AAT	CTT	CGT	AAT	TTA	TAT	TAT	CAG	TAT	AAT	CAG	GTA	TCT	TCT	TCT	146
V	P	R	G	V	F	N	D	L	V	S	V	Q	Y	L	N	L	Q	R	N	166	
GTC	CCG	AGA	GGG	GTA	TTT	AAT	GAT	CCTA	GTT	TCA	GTT	CAG	TAC	TTA	AAT	CTA	CAA	AGG	AAT	632	
R	L	T	V	L	G	S	G	T	F	V	G	M	V	A	L	R	I	L	D	186	
CGC	CTC	ACT	GTC	CTT	GGG	AGT	GGT	ACC	TTT	GTT	GTT	GGT	ATG	GTT	GCT	CTT	CGG	ATA	CTT	GAT	692
L	S	N	N	N	I	L	R	I	S	E	S	G	F	Q	H	L	E	N	L	206	
TTA	TCA	AAC	AAT	AAC	ATT	TTG	AGG	ATA	TCA	GAA	TCA	GGC	TTT	CAA	CAT	CTT	GAA	AAC	CCT	T	752
A	C	L	Y	L	G	S	N	N	L	T	K	V	P	S	N	A	F	E	V	226	
GCT	TGT	TTG	TAT	TGA	GGG	AGT	AAT	AAT	TTA	ACA	AAA	GTA	CCA	TCA	AAT	GCC	TTT	GAA	GTA	812	
L	K	S	L	R	R	L	S	L	S	H	N	P	I	E	A	I	Q	P	F	246	
CTT	AAA	AGT	CTT	AGA	AGA	CTT	TCT	TTG	TCT	CAT	AAT	CCT	ATT	GAA	GCA	ATA	CAG	CCC	TCT	872	
A	F	K	G	L	A	N	L	E	Y	L	L	K	N	S	R	I	R	N	266		
GCA	TTT	AAA	GGA	CTT	GCC	AAT	CTG	GAA	TAC	CTC	CTC	CTG	AAA	AAT	TCA	AGA	ATT	AGG	AAT	932	
V	T	R	D	G	F	S	G	I	N	N	L	K	H	L	I	L	S	H	N	286	
GTT	ACT	AGG	GAT	GGG	TTT	AGT	GGA	ATT	AAT	CCT	AAA	CAT	TTG	ATC	TTA	AGT	CAT	AAT	992		

Fig. 2B

D	L	E	N	L	N	S	D	T	F	S	L	L	K	N	L	I	Y	L	K	306	
GAT	TTA	GAG	AAT	TTA	AAT	TCT	GAC	ACA	TTC	AGT	TTG	TTA	AAG	AAT	TTA	ATT	TAC	CTT	AAG	1052	
L	D	R	N	R	I	I	S	I	D	N	D	T	F	E	N	M	G	A	S	326	
TTA	GAT	AGA	AAC	AGA	ATA	ATT	AGC	ATT	GAT	AAT	GAT	ACA	TTT	GAA	AAT	ATG	GGA	TCT	TCT	1112	
L	K	I	L	N	L	S	F	N	N	L	T	A	L	H	P	R	V	L	K	346	
TG	AAG	AAT	ATC	CTT	AAT	CTG	TCA	TTT	AAT	ATT	CTT	ACA	GCC	TTG	CAT	CCA	AGG	GTC	CTT	AAG	1172
P	L	S	S	L	I	H	L	Q	A	N	S	N	P	W	E	C	N	C	K	366	
CCG	TTG	TCT	TCA	TTG	ATT	CAT	CTT	CAG	GCA	AAT	TCT	AAT	CCT	TGG	GAA	TGT	AAC	TGC	AAA	1232	
L	L	G	I	R	D	W	L	A	S	S	A	I	T	L	N	I	Y	C	Q	386	
CTT	TTG	GGC	CTT	CGA	GAC	TGG	CTA	GCA	TCT	TCA	GCC	ATT	ACT	CTA	AAC	ATC	TAT	TGT	CAG	1292	
N	P	P	S	M	R	G	R	A	L	R	Y	I	N	I	T	N	C	V	T	406	
AAT	CCC	CCA	TCC	ATG	CGT	GGC	AGA	GCA	TTA	CGT	TAT	ATT	AAC	ATT	ACA	AAT	TGT	GTT	ACA	1352	
S	S	I	N	V	S	R	A	W	A	V	V	K	S	P	H	I	H	H	K	426	
TCT	TCA	ATA	AAT	GTA	TCC	AGA	GCT	TGG	GCT	GTT	GTA	AAA	TCT	CCT	CAT	ATT	CAT	CAC	AAG	1412	
T	T	A	L	M	M	A	W	H	K	V	T	N	G	S	P	L	E	N	446		
ACT	ACT	GCG	CTA	ATG	ATG	GCC	TGG	CAT	AAA	GTA	ACC	ACA	ATT	GGC	AGT	CCT	CTG	GAA	ATT	1472	

Fig. 2C

T	E	T	E	N	I	T	F	W	E	R	I	P	T	S	P	A	G	R	F	466
ACT	GAG	ACT	GAG	AAC	ATT	ACT	TTC	TGG	GAA	CGA	ATT	CCT	ACT	TCA	CCT	GCT	GGT	AGA	TTT	1532
F	Q	E	N	A	F	G	N	P	L	E	T	T	A	V	L	P	V	Q	I	486
TTT	CAA	GAG	AAT	GCC	TTT	GGT	AAT	CCA	TTA	GAG	ACT	ACA	GCA	GTG	TTA	CCT	GTG	CAA	ATA	1592
Q	L	T	T	S	V	T	L	N	L	E	K	N	S	A	L	P	N	D	A	506
CAA	CTT	ACT	ACT	TCT	GTG	ACC	TTG	AAC	TTG	GAA	AAA	AAC	AGT	GCT	CTA	CCG	AAT	GAT	GCT	1652
A	S	M	S	G	K	T	S	L	I	C	T	Q	E	V	E	K	L	N	E	526
GCT	TCA	ATG	TCA	GGG	AAA	ACA	TCT	CTA	ATT	TGT	ACA	CAA	GAA	GTT	GAG	AAG	TTG	AAT	GAG	1712
A	F	D	I	L	A	F	F	I	L	A	C	V	L	I	I	F	L	I	I	546
GCT	TTT	GAC	ATT	TTG	CTA	GCT	TTT	TTC	ATC	TTA	GCT	TGT	GTT	TTA	ATC	ATT	TTT	TTG	ATC	1772
Y	K	V	V	Q	F	K	Q	K	L	K	A	S	E	N	S	R	E	N	R	566
TAC	AAA	GTT	GTT	CAG	TTT	AAA	CAA	AAA	CTA	AAG	GCA	TCA	GAA	AAC	TCA	AGG	GAA	AAT	AGA	1832
L	E	Y	S	F	Y	Q	S	A	R	Y	N	V	T	A	S	I	C	N	586	
CTT	GAA	TAC	TAC	AGC	TTT	TAT	CAG	TCA	GCA	AGG	TAT	AAT	GTA	ACT	GCC	TCA	ATT	TGT	AAC	1892
T	S	P	N	S	L	E	S	P	G	L	E	Q	I	R	L	H	K	Q	I	606
ACT	TCC	CCA	AAT	TCT	CTA	GAA	AGT	CCT	GGC	TTG	GAG	CAG	ATT	CGA	CTT	CAT	AAA	CAA	ATT	1952

Fig. 2D

卷之六

V P E N E A Q V I L F E H S A L *	GTT CCT GAA AAT GAG GCA CAG GTC ATT CTT TTT GAA CAT TCT GCT TTA TAA	623 2003
CTCTAACTAATAATTGTCTATAAGAACCTCAGTGGCCATGGACATGATTAAACTGAAACCTCCTTATAATTATAC	2082	
TTTAGTGGAAATATAATGAATTATGAGGTTAGCATTATAAATATGTTTAATAAAAAAAAAAAAAGG	2161	
GGGGCGCG		2169

Fig. 2E

ESTATE TRUSTS

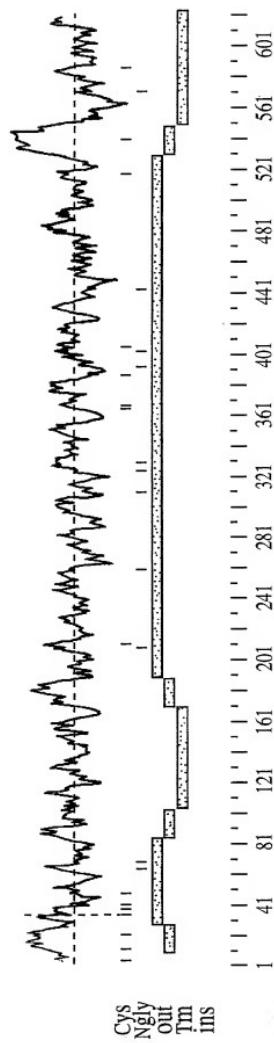


FIG. 2F

T. G. E. F. T. L. I. = T. G. S. S. L. E. I.

Slit	MRGVGQMLSLIGLVLA	10	20	30	40	50	60
:	: :	:	:	:	:	:	
325	MCGLQFSLPCRLRFLVVTCYLLLHK-E	10	20	30	40	50	60
Slit	NNITRITKTDFAGLRHLRVQLMENKISTIERGAFQDLKELERIRLNRNHQLFPEELLFGTAKLYRLDL	70	80	90	100	110	120
:	:	:	:	:	:	:	
325	NNISYINESELTGELHSVALYLDNSNLIYVYPKAFAQVQLR-----	70	80	90	100	110	120
Slit	SENQIQAIPRKAFRGAVDIKNLQLDYNQNSCIEDGAFAFLRDLEVLTLNNNNNITRLSYASFNHMPKLRTF	140	150	160	170	180	190
:	:	:	:	:	:	:	
325	-----PGI-----PKGLINLRNLQYNOVSFVPRGVFNDLVSVQYLNLRNRLTVLGSGTF-----	130	140	150	160	170	
Slit	RIHSNNNLYCDCHIAWLSDWLRQRPRVGLYTQCMGPSHLRGHNVAEVQKREFVCSSHQSFMAPSCSVLHCP	210	220	230	240	250	260
:	:	:	:	:	:	:	
325	-----VGM-----VA-----						180

Fig. 2G

Slit AACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEQNTIKVPPGAAFSPPYKKLRRIDLDSNNQISELAPDAF
 325 -----
 Slit QGLRSLNLSLVLYGNKITELPKSLFEGLFLSQQLLLNANKINCLRDAFQDLHLNINLLSLYDNKLQTIAKG
 350 360 370 380 390 400 410
 :::
 325 -LR----- ISE-----
 325 -----
 Slit TFSPLRAlQTMHIAQNPFICDCHIKWLADYLHTNPIETSGARCTSPRLANKRIGQIKSKKFRGSAKEQY
 420 430 440 450 460 470 480
 :::
 325 -----
 Slit FIPGTEDYRSKLSGDCFADIACPEKRCGEFTVDCSNQQLNKLPEHIFQYTAELRNNEFTLEATGIF
 490 500 510 520 530 540 550
 :::
 325 -----
 190
 200
 210
 220

Fig. 2H

卷之三

560	570	580	590	600	610	620
Slit	KKL PQLRKINFSSNNKITDIEGEGASSGVNEILLTSNRLENVOHHMFKGLESI	KTLMLRSNRITCVGND				
325	----LRRRLSIIHNPPIEAIQ--PFA-----	-----	-----	-----	-----	
	230	240				
630	640	650	660	670	680	690
Slit	SFIGLSSVRLLSLYDNQITTVAPGAFDTLHSLSLNLANPFNCNCYLAWLGEWLKKRIVTGNPRCQKP					
325	GFGGINNLKHLILSHND-----	LEN-----	LEN-----	LEN-----	LEN-----	
	280	290	290	290	290	
700	710	720	730	740	750	760
Slit	YFLIKEIPIQDVAIQDFTCDDGNDDNSCSFLSRCPTECTCLDTIVRCNSNKGKVLPKGIPRDVTEYL	DGN				
325	-----	-----	-----	-----	-----	
770	780	790	800	810	820	830
Slit	QFTLVPKELSNYKHHTLIDLSNNRILSTLNQSFSNM-TQLLTLLSYNRLRCIPRTFDGLKSLRLLSLH					
325	TFSSL-----KNLIYKLDRNRIISIDNTFENMGASLKLNLNFNNLTLAHPRV--LKPL-----					
	300	310	320	330	340	

Fig. 2I

840 850 860 870 880 890 900
 Slit GNDISVVPEGAFNDLISALSHLAIGANPLYCDCNMQWLSDWVKSEYKEPIARCAAGPGENADMKLLTPSK
 ::::: ::::: ::::: ::::: :::::
 325 -----SSLHLQANSNWEWCNCNLIGLIRDWLAS-----
 350 360 370

 910 920 930 940 950 960 970
 Slit KFTCQGPVDVNLAKCNPCLSNPCKNDGTCNSDPVDFYRCTCPYGFQGQDCDVPIHACISNPCKHGGTCH
 ::::: :::::
 325 -----SAITLN-----
 380

 980 990 1000 1010 1020 1030 1040
 Slit LREGEEDGFWCICADGFEGENCEVNDDCEDNDCEENNSTCVDGINNYTCLCPPEYTGLCEEKLDFCQAQD
 ::::: :::::
 325 -----RALKYI-----
 400

 1050 1060 1070 1080 1090 1100 1110
 Slit INPCQHDSKCLTPKGFKCDCTPGYVGEHCDIDFDDQDNKCKNGAHCDAVNGTCICPEGYSGLFCEF
 :::::
 325 -----TSSIN-----
 410

Fig. 2J

1120 1130 1140 1150 1160 1170 1180
 Slit SPPMVLPRTPSPCDNFDCQNGAQCIVRINEPICQCLPGYQGEKCEKLVSVNFINKESYLQIPSASKVRPQTN
 :: . .
 325 ----VSRAWA-----VVK-----
 420 430

1190 1200 1210 1220 1230 1240 1250
 Slit ITIQUIATEDSSGILLYKGDKDHIAVELYGRVRAASYDTGSHPASALYSVETINDGNFHIVELIALDQSLS
 :: . .
 325 ----TTNGSP---LENTEINIT---FWERIPTS----PAGREFQENAFGNPN-LETTAVILPVQIQLT
 440 450 460 470 480

1260 1270 1280 1290 1300 1310 1320
 Slit LSVDGGNPKITNISKOSTLNFDSPLYVGGAPGKSNVASLRQAPGQNGTSFHGCIRNLTYINSELQDFQKV
 :: . .
 325 TSV-----TINLEKNSALPNDAA---SMSGKTSLI-----CT-----QEVEKL
 490 500 510 520

1330 1340 1350 1360 1370 1380 1390
 Slit PMQTGILPGCEPCHKVKCAHGTQPSQAGFTCECQEWMGPLCDQRTNDPCILGNKCVHGTCLPINAFSY
 :: .
 325 NEADILLA-----F-----FIL

Fig. 2K

E-GSPTTQ: TITSEGZ-ESD

1400	1410	1420	1430	1440	1450	1460
S11t SCKCLEGHGGVILCDEEEEDLFNPQCQAIKCKHGKCRLSGLGOPYCECSGYTGDSCLREISCRGERIRDYYQ						
⋮	⋮	⋮	⋮	⋮	⋮	⋮
325 AC-----VL-----IIFLIYKVVQFFQ---KLKA-----SENS-----RENRL-EYY-						
540	550	560	570			
1470	1480	1490	1500	1510	1520	
KQQGYAACQTTK-KVSRLECRGGCAGGCCGPLRSKRKYSFECTDGSSFVDEVVKVKCGCTRCVS						
⋮	⋮	⋮	⋮	⋮	⋮	
325 ---SF--YQOSARNVNTASICNTSPNSLESPGLEQIRLHK-----QIVPNEAQVVI-LFEHSAL						
580	590	600	610	620		

Fig. 2L

Y G G T T G G : T T C G G A G G G

Slit 10 20 30 40 50 60 70
CAGGAGGGTGGAGGGCGGTGGAGCGCTGAGTGGCTACTGCCCTGTTCCATTATT

325 -----

Slit 80 90 100 110 120 130 140
TTGTGCACATTTCCCTGGCACTCTGGTTGCTAGCCCCGGGAAGTGCCCTCAGACACTGCCGGT

325 -----

Slit 150 160 170 180 190 200 210
TCCCTCGGAGCAAGCTAAAGAAAAGCCCCAGTGCCGGCAGGAAGGGGGAAAAGATGCGC

325 -----

Slit 220 230 240 250 260 270 280
GGCGTTGGCTGGCAGATGCTGTCCTGTCGGTTAGTGTGGATCCTGAAAGGTGGCACCGC

325 -----

GTGCG-----ACC-----
:::
:::
:::

Fig. 2M-1

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Fig. 2M-2

TGTGTTTGCTGGACTCTGGGAACTGCGAAGCTATACAGGGCTGATCTCAGTGAATAACCAATTCAAGGCAATC

Slit 570 580 590 600 610 620 630
 : ::::::: : ::::::: : ::::::: : ::::::: : ::::::: : ::::::: : ::::::: : ::::::: : :::::::
 325 T-----TTTCCTTG---C---CAATTCGTATCTGA-----ACAGA-AAATCCAAGAACAGG-----
 90 100 110 120 130

Slit 640 650 660 670 680 690 700
 CCAAGGAAAGCTTCCGTGGGCCAGTTGACATAAAAAAATTGCAACTGGATTACAAACAGATAGCTGTA
 : ::::::: : ::::::: : ::::::: : ::::::: : ::::::: : ::::::: : ::::::: : :::::::
 325 -----GATATGTG-----TGGATTACA-----GTT
 140 150

Slit 710 720 730 740 750 760 770
 TTGAAAGATGGGCATTAGGGGCTCTCCGGACCTGGAAAGTGTCACTCTCAACAAATAACAACTTACTAG
 : ::::::: : ::::::: : ::::::: : ::::::: : ::::::: : ::::::: : :::::::
 325 TT-----CTCT-----GCCT-----TGC-----CTACGA-----
 160 170 180 190 200

Slit 780 790 800 810 820 830 840
 ACTTTCTGTGGCAAAGTTCAACCATATGGCTAAACTTAGGACTTTTGACTGCATTCAACAAACCTGTAT
 : ::::::: : ::::::: : ::::::: : ::::::: : ::::::: : :::::::
 325 -----CTGTTTCIGGGTGTACCTGTTA-----TCTTT-----AT
 180 190 200

Fig. 2M-3

Slit	TGTGACTGCCACACTGGCCTGGCTCTCCGACTGGCTTCGCCAAAGGCCCTGGGTGGTCTGTACACTCAGT	850	860	870	880	890	900	910
325	TATTACT-CCACAAAG-----	210			:::	:::	:::	:::
					AAATAC-----	-----TGGGA-TGTTCG-TC--T		
					220		230	
Slit	GTATGGCCCCCTCCCACCTGGAGGGCCATAATGTAGCTGAGGTTCAAAAAAGGAAATTGGCTGAGTGG	920	930	940	950	960	970	980
325	GTTTG-----TC-----	240			:::	AGC-----		
					250			
Slit	TCMCCAGCATTATGGCTCTTGTAGIGTTTGCCTGCCCTGGCCCTGGTAGCAACAAAT	990	1000	1010	1020	1030	1040	1050
325	G----AGACAAATT-----	260			:::	ACTGCC-----		
					270			
Slit	ATCGTAGACTGTGCGGAAAGGTCTCACTGAGATCCCACAAATCTCCAGA GACCATCACAGAAATAC	1060	1070	1080	1090	1100	1110	1120
325	-----CTTTCGAG----TATTIC----CTAAGA-----	290			:::	-----ATTTCCTGAAA-----GT-ACAGTTTTTC		
					310		320	

Fig. 2M-4

TGGCTTGATGTTGAACTGAA

Slit	1130	1140	1150	1160	1170	1180	1190
	GT	TG	GA	AC	AG	CA	AA
Slit	325	---	TGT	TCTG	-----	-----	-----
	330		340	350	360	370	
Slit	1200	1210	1220	1230	1240	1250	1260
	TG	AC	CTG	GAA	TAAT	CAGAT	TCTGAA
Slit	325	---	CTTGT	-----	-----	-----	-----
	390						
Slit	1270	1280	1290	1300	1310	1320	1330
	CT	TG	CCT	TGAA	AAATAA	CACAGAA	CTCCCCAA
Slit	325	CTTGT	-----	-----	-----	-----	-----
	390						
Slit	1340	1350	1360	1370	1380	1390	1400
	TC	CTT	ATT	TGAA	AAACAAGATA	AACTGCCTTCGGGTAGATGCTT	CAGGATCTCCACAACTTGAA
Slit	430	TTCTGT	TGAT	TAT	CCAAA	-----	-----
	440						

Fig. 2M-5

Slit	CCTTCTCCCTATATGACAACAAGCTCAGACCATGCCAAGGGGACCTTTACCTCTGGGCCATT	1410	1420	1430	1440	1450	1460	1470
	:::: :::: :::	470	480	490	500	510	520	530
Slit	CAAACATGATTGGCCAGAACCCCTTATTGTGACTGCCATCTAAAGTGGCTAGGGATTATCTCC	1480	1490	1500	1510	1520	1530	1540
	:::: :::: :::	500	510	520	530	540	550	560
Slit	ATACCAACCGATTGAGACCAGTGTGCCCGTTGCACAGCCCCCGCTGCCAACAAAAGAATTGG	1550	1560	1570	1580	1590	1600	1610
	:::: :::	540	550	560	570	580	590	600
Slit	ACAGATCAAAAGCAAGAAATTCCCGTTGTTAGCTAAAGAACAGTTTCATTCCAGGTACAGGAATTAT	1620	1630	1640	1650	1660	1670	1680
	:::: :::: :::	560	570	580	590	600	610	620
Slit	ACAGT--ATAATCAGGTA--TCTTTGTTG--CGAGAGG--AGTATTTAAT--	325						

Fig. 2M-6

1690 1700 1710 1720 1730 1740 1750
 Slit CGATCAAAATTAAAGTGGAGACTGCTTGCGGATCTGGCTTGCCCTGAAAAGTGTGCTGTGAAGGAAACCA
 ::::: :::::
 325 -GATCTAGTTT-----CAGTTTCAAG-----
 600 610

1760 1770 1780 1790 1800 1810 1820
 Slit CAGTAGATTGCTCTAATCAAAGCTAACAAAATCCCCGGAGCACATTCCCCCAGTAACACTGCAGAGTTGCG
 ::::: :::::
 325 -----TACITAATCTA-----CAA-----GGAA-----TCGCCT-----CACTG-----
 620 630 640

1830 1840 1850 1860 1870 1880 1890
 Slit TCTCAATAATAATGAAATTACCGTGTGGAAAGGCCACAGGAATCTTTAGAAAACCTCTCAATTACGTAAA
 ::::: :::::
 325 -----TCC---TTGGAG----TGG-----TACCT-----
 650 660

1900 1910 1920 1930 1940 1950 1960
 Slit ATAAAACTTTAGCAACATAAGATCACAGATTGAGGAGGAGCATTTGAAGGGACATCTGGTTAAATG
 ::::: :::::
 325 -----TGTGTTGGTATGGTTGCT-----CTTCGG-----
 670 680

Fig. 2M-7

T G C T T G A T G T T G A C C A T G A A G C A T G A A T C G A G T A A T C G T G T G G A A A T G T G C A G C A T A A G A T G T T C A A G G A T T G G A A A G G C T C A A
 Slit :
 325 --ATACTT---GATTTATC-----A----- 690

1970 1980 1990 2000 2010 2020 2030

Slit :
 325 AAC-----ATAAC--ATTGGAGGATATCAGAATCAG----- 700

2040 2050 2060 2070 2080 2090 2100

Slit :
 325 -----:-----:-----:-----:-----:-----:----- 710

2110 2120 2130 2140 2150 2160 2170

Slit :
 325 -----:-----:-----:-----:-----:-----:----- 720

2180 2190 2200 2210 2220 2230 2240

Slit :
 325 -----AACATCTTGAA-AAA CCTT-----:-----:-----:-----T----- 730

Fig. 2M-8

T T G G A A G G A A T T G T C A C G G G A A T C T A G A T G T A A A A C C A T G A A G G A A T A C C C A T C

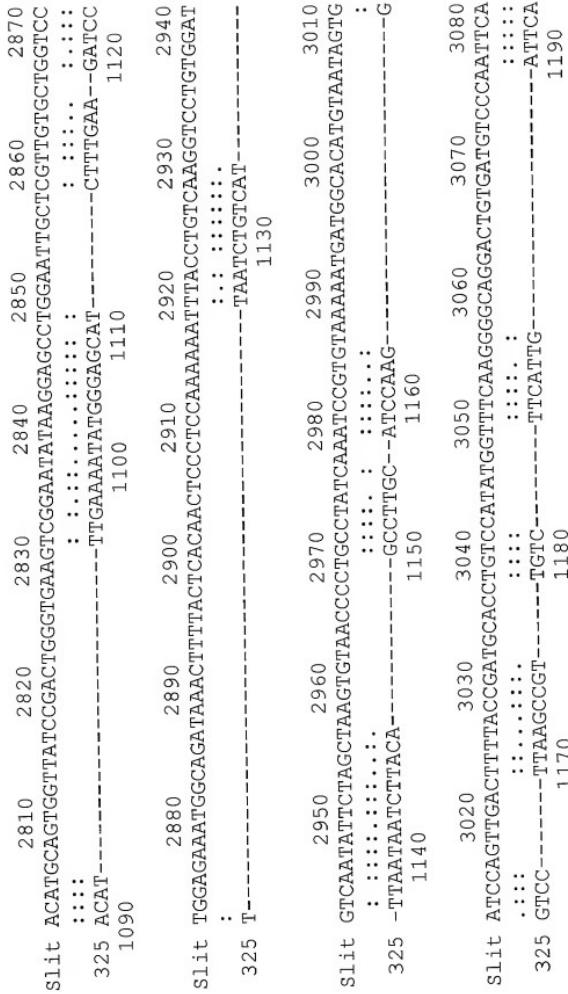
Slit	2250	2260	2270	2280	2290	2300	2310
	GAGAAAGAGAAATTGTCTACGGGAATCTAGATGTTAAAACCATACTTCCTGAAAGAAATACCCATC						
	::	::	::	::	::	::	::
325	TAGGAAGTAAATTAA	TTA--ACAAAGTAC	-----	ATCAAATGCCTT	-----	-GAAGTAC	-----
	780	790	800	810			
	780	790	800	810			
Slit	2320	2330	2340	2350	2360	2370	2380
	CAGGATGTGGCATTCAAGGACTTCACTTGATGACGGAAATGACAATAGTGTGCTCCCCACCTTCTC						
	::	::	::	::	::	::	::
325	-----	TTAAAAGTCTT	-----	-----	-----	-----	-----
				AGAACCTTT	-----	CTTTGTCTC	
				830		840	
				820			
Slit	2390	2400	2410	2420	2430	2440	2450
	GCTGCTCTACTGAATGTAATGCTGGATACAGTCGTCGGATGTGAAACAAGGGTTGAAGGTCTTGCC						
	::	::	::	::	::	::	::
325	ATAATCCTATTGAA	-----	GCA--ATACAG-C	--CCCTTG	--CA	-----	-----
	850	860	870	870	880	890	
	850	860	870	870	880	890	
Slit	2460	2470	2480	2490	2500	2510	2520
	GAAAGGTATTCCAAGAGATGGTCACAGAGTTGATCTGGATGGAAAQCATTACACTGGTTCCAAGGAA						
	::	::	::	::	::	::	::
325	AA-----	-----	-----	TCTGGA	-----	ATACCC	-----
				900		TCC	-----

Fig. 2M-9

TTGCTTGATTTTGTGAAAGAATTAAT

	2530	2540	2550	2560	2570	2580	2590
Slit	CTCTCCAACTACAAACATTAAACACTTAAAGCTTAACTTAAAGTAACTTAAAGTAACAGAACAGAACATGTTCTTAATCAGA						
	325	325	325	325	325	325	325
	TCCTGAAATTCAAGAA	TCCTGAAATTCAAGAA	TCCTGAAATTCAAGAA	TCCTGAAATTCAAGAA	TCCTGAAATTCAAGAA	TCCTGAAATTCAAGAA	TCCTGAAATTCAAGAA
	910	920	930	940	950	960	970
	2600	2610	2620	2630	2640	2650	2660
Slit	GCTTCAGCAACATGACCCAGCTCCTCACCTTAATTCTTAGTTACACCGTCTGAAGATGTATTCTCCCTCG						
	325	325	325	325	325	325	325
	AATTAATAATCTTAA	AATTAATAATCTTAA	AATTAATAATCTTAA	AATTAATAATCTTAA	AATTAATAATCTTAA	AATTAATAATCTTAA	AATTAATAATCTTAA
	970	980	990	1000	1010	1020	1030
	2670	2680	2690	2700	2710	2720	2730
Slit	CACCTTGTGATTAAAGTCTCTTGATGTTACTCTTCTACATGGAAATGACATTCTGTTGTGCCTGAA						
	325	325	325	325	325	325	325
	TTTAGAGAAATTAAAT	TTTAGAGAAATTAAAT	TTTAGAGAAATTAAAT	TTTAGAGAAATTAAAT	TTTAGAGAAATTAAAT	TTTAGAGAAATTAAAT	TTTAGAGAAATTAAAT
	1060	1070	1080	1090	1100	1110	1120

Fig. 2M-10

**Fig. 2M-11**

Slit TGCTGATCAGTAACCATGTAAACATGGAGGAACATTGCCACTTAAAGGAGAAGGATGGATT
 : ::::: :::::
 325 T-----CTTACGG----CAAATT-----CTAAC-T-CTT-----GGAATGTAACCTGAAAC
 3090 3100 3110 3120 3130 3140 3150
 Slit TGGGTGATTTGCTGATGGATTGAAAGGAGAAAATTGTAAGTCACGTTGATTTGAAAGATAATG
 : ::::: :::::
 325 T-----TTTGGGC-----CTTCA-----G
 3160 3170 3180 3190 3200 3210 3220
 Slit ACTGTGAAATAATTCTACATGTGATGGCATTAAACTACACATGCCCTTGCCACCTGAGTATAC
 ::::: :::::
 325 ACTG-----GC-----TAGCAT-----GCCATTAC-----
 3230 3240 3250 3260 3270 3280 3290
 Slit AGGTGAGTTGTTGAGGAAGCTGGACTTCTGCCCCAGGACCTGAAACCCCTGCCAGCACGATTCAAAG
 ::::: :::::
 325 -----TCTAAACATCTATT-----GTCAAGAACCCCC-----
 1240 1250 1260 1270 1280 1290

Fig. 2M-12

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Fig. 2M-13

Fig. 2M-14

Τ θεωρείται πιο σημαντικό

Slit	3930	3940	3950	3960	3970	3980	3990
	CTTCCACATTTGGAACTACTTGCCTTGATCAGAGTCCTCTTGTCCGTTGGATGGTGGAAACCCAAA						
325	CTACCG--AATGATGCTGCTT-----		CAATGTC-----		AGGGAA-----		
	1640	1650			1660		
Slit	4000	4010	4020	4030	4040	4050	4060
	ATCATCACTAACCTTGTCAAAGCAGTCCACCTGGAATTGACTCTCACTCTATGTAGGGCATGCCAG						
325	AACATCTAAATTGTT-----		ACACAAAGATTGAA-----				
	1670	1680			1690		
Slit	4070	4080	4090	4100	4110	4120	4130
	GGAAGAGTAACGTGGCATCTTGCGCCAGGCCCTGGCAGAACGGAACAGCTCCACGGCTGCATCCG						
325	-GAAGTTGAATGAGGGTT-----		TGACATTTG---CTAGCTT-----				
	1700	1710			1720		
Slit	4140	4150	4160	4170	4180	4190	4200
	GAACCTTTACATCAACAGTGGAGCTGCAGGACTTCCAGAAAGGTGCCATGGCAAAACAGGCATTGGC						
325	----TTTCATC---TTAGCTT-----		GTG-----TTTAATCATTT-----				
	1740				1750		1760

Fig. 2M-15

TGTGAGCCATGCCAACAGGGTGTGCCATGGCACATGCCAGCCAGCAGCAGGCTTCACCT
 Slit 4210 4220 4230 4240 4250 4260 4270
 : : : : : : : :
 325 TTGATC--TAC-----AAGTTGTT-----CAGTTA---A
 1770 1780 1790

GCGAGTGCCAGGAAGGATGGATGGGGCCCTCTGTGACCAACGGACCAATGACCCCTTGCAAATAA
 Slit 4280 4290 4300 4310 4320 4330 4340
 : : : : : : : :
 325 ACAAAACTA--AAGG-----CATCAGAAAAT-----CAAGGGAAAT
 1800 1810 1820

ATGCGTACATGGCACCTGCTTGCCCCATCAATGCGTTCTCCCTACAGCTGTAAGTGTGGGGCCATGGA
 Slit 4350 4360 4370 4380 4390 4400 4410
 : : : : : : : :
 325 AGACTTGAATA-CTACAGCT-----TTATCAGTAGGAAAGTATA-----ATGTA
 1830 1840 1850 1860 1870

GGTGTCCTCTGTGATGAAGAGGGATCTGTTAACCATGCCAGGGATCAAGTGCAGCACGGGAAGT
 Slit 4420 4430 4440 4450 4460 4470 4480
 : : : : : : : :
 325 ACTG-CCTCAAT-TTG-----TAACACTTCCC-----CAAAATTCT-CT-AGAAAGT
 1880 1890 1900 1910

Fig. 2M-16

Slit GCAGGCTTTCAGGTGGGGAGCCCTACTGTGAATGCCAGTGATAACACGGGGACAGCTGTGATCG
 4490 4500 4510 4520 4530 4540 4550
 :::::
 325 CCTGGCTT-----GGAGCAG-----ATTCA-----GACTCA-TAAACA
 1920 1930 1940

Slit AGAAATCTCTTGTGAGGGAAAGGATAAGAGATTATACCAAAAGCAGCAGGGCTATGCTTGCTTGC
 4560 4570 4580 4590 4600 4610 4620
 :::::
 325 AATGT-TC-----C-----TGAAAATGAG-----GCA-CAGGTC-AATCTTTTG---A
 1950 1960 1970 1980

Slit ACAACCAAGAAGGTGTOCCGATTAGAGTGGCAGAGGTGGGTGTGAGGGCAGTGCCTGGACCGCTGA
 4630 4640 4650 4660 4670 4680 4690
 :::::
 325 ACATTC-----
 1990

Slit GGAGCAAGCGGGAAATACTCTTTCGAATGCACTGACGGCTCCTCTGTGGACGAGGTGAGAAAGT
 4700 4710 4720 4730 4740 4750 4760
 :::::
 325 --AACTAA-----ATATTGTCTATAAGAAACT---TCAGTGCA-----TGGACATGATTAAA-----
 2010 2020 2030 2040 2050

Fig. 2M-17

Slit GGTGAAGTGGCGCTGTACGAGGTGTGCTAACACACTCCGGCAGCTCTGTCCTTTGGAAAAGGTTG
 4770 4780 4790 4800 4810 4820 4830
 :::
 325 -----CTG-----AAAC---CTC-----CTT---ATAATAATTA
 2060 2070

Slit TATACTTCTGACCATGGGACTAATGAATGCTTCATAGTGGAAATTGAAATATTTGAAATAATTTGAAATAAC
 ::::::: .:. :: .:. ::::: .:. :: .:. :: .:. :: .:. :: .:
 325 TATACTT-TAGT-----TGGAAATAATAATGGATTATATGAGGTAGCATTATTAAATATGTTTTAA----
 2080 2090 2100 2110 2120 2130 2140 2150 2160

Slit AGAACAGACTTATTTTATTATGAGAATAAGACTTTTTCTGCATTG
 ::-----TAAAAAAAAAGGGCG-----GCCGC-----
 4910 4920 4930 4940 4950

Fig. 2M-18

M	P	L	S	L	G	A	E	M	W	G	P	E	A	W	L	L	L	L	L	20
ATG	CCC	TCC	CTG	GGG	GAG	TGG	GGG	CCT	GAG	GCC	TGG	CTG	CTG	GAC	GTG	CTG	CTG	CTG	CTA	294
L	L	A	S	F	T	G	R	C	P	A	G	E	L	E	T	S	D	V	V	40
CTG	CTG	GCA	TCA	TTT	ACA	GCG	CGG	TGC	CCC	GCG	GGT	GAG	CTG	GAG	ACC	TCA	GAC	GTG	GTA	354
T	V	V	L	G	Q	D	A	K	L	P	C	F	Y	R	G	D	S	G	E	60
ACT	GTG	GTG	CTG	GGC	CAG	GCA	AAA	CTG	CCC	TGC	TTC	TAC	CGA	GGG	GAC	TCC	GCG	GAG	414	
Q	V	G	Q	V	A	W	A	R	V	D	A	G	E	G	A	Q	E	L	A	80
CAA	GTG	GGG	CAA	GTG	GCA	TGG	GCT	CGG	GTG	GAC	GCG	GGA	GCC	CAG	GAA	CTA	GCG	474		
L	L	H	S	K	Y	G	L	H	V	S	P	A	Y	E	G	R	V	E	Q	100
CTA	CTG	CAC	TCC	AAA	TAC	GGG	CTT	CAT	GTG	AGC	CCG	GCT	TAC	GAG	GGC	CGC	GTG	GAG	CAG	534
P	P	P	R	N	P	L	D	G	S	V	L	L	R	N	A	V	Q	A	120	
CCG	CCC	CCA	CGC	AAC	CCC	CTG	GAC	GGC	TCA	GTG	CTC	CTG	CGC	AAC	GCA	GTG	CAG	GCG	594	

Fig. 3A

D	E	G	E	Y	E	C	R	V	S	T	F	P	A	G	S	F	Q	A	R	140
GAT	GAG	GCG	GAG	TAC	GAG	TGC	CGG	GTC	AGC	ACC	TTC	CCC	GCC	GGC	AGC	TTC	CAG	GCG	CGG	654
L	R	L	R	V	L	V	P	P	L	P	S	L	N	P	G	P	A	L	E	160
CTG	CGG	CTG	CTG	CGA	GTG	GTG	CCT	CCC	CTG	CCC	TCA	CTG	AAT	CCT	GGT	CCA	GCA	CTA	GAA	714
E	G	Q	G	L	T	L	A	A	S	C	T	A	E	G	S	P	A	P	S	180
GAG	GGC	CAG	GGC	CTG	ACC	CTG	GCA	GCC	TCC	TGC	ACA	GCT	GAG	GGC	AGC	CCA	GCC	CCC	AGC	774
V	T	W	D	T	E	V	K	G	T	T	S	S	R	S	F	K	H	S	R	200
GTG	ACC	TGG	GAC	AGC	GAG	GTC	AAA	GGC	ACA	ACG	TCC	AGC	CGT	TCC	TTC	AAG	CAC	TCC	CGC	834
S	A	A	V	T	S	E	F	H	L	V	P	S	R	S	M	N	G	Q	P	220
TCT	GCT	GCC	GTC	ACC	TCA	GAG	TTC	CAC	TTG	GTG	CCT	AGC	CGC	AGC	ATG	AAT	GGG	CAG	CCA	894
L	T	C	V	V	S	H	P	G	L	Q	D	Q	R	I	T	H	I	L	240	
CTG	ACT	TGT	GTG	GTG	TCC	CAT	CCT	GGC	CTG	CTC	CAG	GAC	CAA	AGG	ATC	ACC	CAC	ATC	CTC	954
H	V	S	F	L	A	E	A	S	V	R	G	L	E	D	Q	N	L	W	H	260
CAC	GTG	TCC	TTC	CTT	GCT	GAG	GCC	TCT	GTG	AGG	GGC	CTT	GAA	GAC	CAA	AAT	CTG	TGG	CAC	1014
I	G	R	E	G	A	M	L	K	C	L	S	E	G	Q	P	P	S	Y	280	
ATT	GGC	AGA	AGA	GGA	GCT	ATG	CTC	AAG	TGC	CTG	AGT	GAA	GGG	CAG	CCC	CCT	CCC	TCA	TAC	1074

Fig. 3B

TGG TGT GAG GAT GAA GTC CCA CGG

N	W	T	R	L	D	G	P	L	P	S	G	V	R	D	G	D	T	L	300	
AAC	TGG	ACA	CGG	CTG	GAT	GGG	CCT	CTG	CCC	AGT	GGG	GTA	CGA	GTG	GAT	GGG	GAC	ACT	TTG	1134
G	F	P	P	L	T	T	E	H	S	G	I	Y	V	C	H	V	S	N	E	320
GGC	TTT	CCC	CCA	CTG	ACC	ACT	GAG	CAC	AGC	GGC	ATC	TAC	GTC	TGC	CAT	GTC	AGC	AAT	GAG	1194
F	S	S	R	D	S	Q	V	T	V	D	V	L	D	P	Q	E	D	S	G	340
TTC	TCC	TCA	AGG	GAT	TCT	CAG	GTC	ACT	GTG	GAT	GTT	CTT	GAC	CCC	CAG	GAA	GAC	TCT	GGG	1254
K	Q	V	D	L	V	S	A	S	V	V	V	V	G	V	I	A	A	L	L	360
AAG	CAG	GTG	GAC	CTA	GTG	TCA	GCC	TCG	GTG	GTG	GTG	GGT	GTG	ATC	GCC	GCA	CTC	TGT	1314	
F	C	L	L	V	V	V	L	M	S	R	Y	H	R	R	K	A	Q	380		
TTC	TGC	CTT	CTG	GTG	GTG	GTG	GTG	CTG	TCC	ATG	TCC	CGA	TAC	CAT	CGG	CGC	AAG	GCC	CAG	1374
Q	M	T	Q	K	Y	E	E	L	T	L	T	R	E	N	S	I	R	R	400	
CAG	ATG	ACC	CAG	AAA	TAT	GAG	GAG	CTG	ACC	CTG	ACC	AGG	GAG	AAC	TCC	ATC	CGG	AGG	1434	
L	H	S	H	H	T	D	P	R	S	Q	P	E	E	S	V	G	L	R	A	420
CTG	CAT	TCC	CAT	CAC	ACG	GAC	CCC	AGG	AGC	CAG	CCG	GAG	GAG	AGT	GTA	GGG	CTG	AGA	GCC	1494
E	G	H	P	D	S	L	K	D	N	S	S	C	S	V	M	S	E	E	P	440
GAG	GGC	CAC	CCT	GAT	AGT	CTC	AAG	GAC	AAC	AGT	AGC	TGC	TCT	GTG	ATG	AGT	GAA	GAG	CCC	1554

Fig. 3C

Fig. 3D

TCAAGGAATCCCTCGCCTCAGCCTCCCTAGTAGCTGGACTTAAAGTGACCAACTGTGCCCTGCCTTGAATCCCTTA 2715
 CGAAGAGAAAAAAATAAGAAAAGGCCCTTAGATTATCCAATGTTACTACTGGATITGGTAAAGTGAGGCCCT 2794
 CAAACACCAGGGGTTAACCTGTGATITGGTAAAGGGGCTACTCCAAGGCACTTCAGGGCATCTCAAGGCAAGCCCTGGGAG 2873
 GGCACCTGAGAGCTGGTAGAGCTGCTGAAATTAGGGATGTGAGCTCGTGGTTACTGAGTAAGGTTAAATTGCATCCACCA 2952
 TTGGTTTGATACCTTGGGAATTGCTTGAACCTGGTGAAGGTCTCTGTCATAGTGGTGTGGAGAGAGAGA 3031
 GCAGTGATTATAAGCCGAGAGTAGGAGTGGAGTGGGTGAGGTGAAGGGTCTGGGGGTGAGAATGTCGCCCTTCCCCC 3110
 TGGGTTTGATCACTAATTCAAGGTCTTCTGGATGTTCTGGTTCTGGTTGGCTGGAGTCAATGAGTTTATTTTTA 3189
 GCTGGCCCAACCAAGATAACACTCAGCCAGATAACCTAGATTAGTACCAACTCTTCTAGTCTGAATCTGGATT 3268
 TCTGGCCCTAAGGGAGGGCTCCCATCCTCTGGTCCCCAGCCAGCTTAGGACTCGAATGGGGCTGAAGATCTAAGA 3347
 TCCTAAACATGTAATTTTATGTAATAATGTGATATTGTACATAAAATGATATTCTGTTTAATAAAGACAGACAAAA 3426
 CTTGAAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....
 AAAAAA 3505
 AAAAAA 3510

Fig. 3E

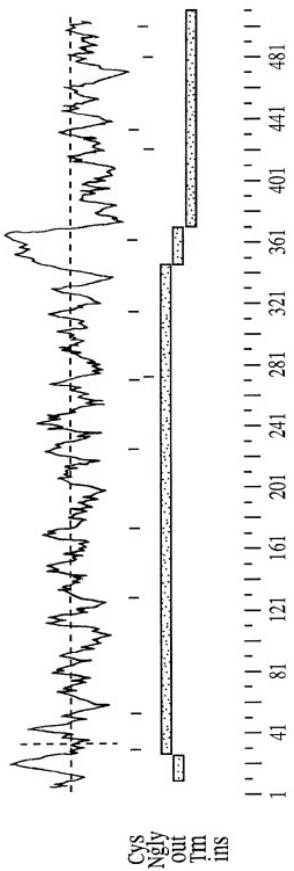


FIG. 3F

K	G	T	T	S	S	R	F	K	H	S	R	S	A	A	V	T	S	19	
C	AAA	GGC	ACA	ACG	TCC	AGC	CGT	TTC	AAG	CAC	TCC	CGC	TCT	GCT	GCC	GTG	ACC	TCA	58
E	F	H	L	V	P	S	R	S	M	N	G	Q	P	L	T	C	V	V	39
GAG	TTC	CAC	TTG	GTG	CCT	AGC	CGC	AGC	ATG	AAT	GGG	CAG	CCA	CTG	ACT	TGT	GTG	TCC	118
H	P	G	L	L	Q	D	Q	R	I	T	H	I	L	H	V	S	F	L	59
CAT	CCT	GCG	CTG	CTG	CTG	CAG	GAC	CAA	AGG	ATC	ACC	CAC	ATC	CTC	CAC	GTG	TCC	TTC	178
E	A	S	V	R	G	L	E	D	Q	N	L	W	H	I	G	R	E	G	79
GAG	GCC	TCT	GTG	AGG	GGC	CTT	GAA	GAC	CAA	AAT	CTG	TGG	CAC	ATT	GGC	AGA	GAA	GCT	238
M	L	K	C	L	S	E	G	Q	P	P	P	S	Y	N	W	T	R	L	99
ATG	CTC	AAG	TGC	CTG	AGT	GAA	GGG	CAG	CCC	CCT	CCC	TCA	TAC	AAC	TGG	ACA	CGG	CTG	298
G	P	L	P	S	G	V	R	V	D	G	D	T	L	G	F	P	P	D	119
GGG	CCT	CTG	CCC	AGT	GGG	GTA	CGA	GTG	GAT	GGG	GAC	ACT	TTG	GGC	TTT	CCC	CCA	CTG	358
T	E	H	S	G	I	Y	V	C	H	V	S	N	E	F	S	S	R	D	139
ACT	GAG	CAC	AGC	ATC	TAC	GTC	TGC	CAT	GTC	AGC	AAT	GAG	TTC	TCC	TCA	AGG	GAT	TCT	418
Q	V	T	V	D	V	L	A	D	P	Q	E	D	S	G	K	Q	V	D	159
CAG	GTC	ACT	GTG	GAT	GTT	CTT	GCA	GAC	CCC	CAG	GAA	GAC	TCT	GGG	AAG	CAG	GTG	GAC	478

Fig. 3G

V	S	A	S	V	V	V	G	V	I	A	A	L	F	C	L	L	V	179
GTG	TCA	GCC	TCG	GTG	GTG	GTG	GTG	GGT	GTG	ATC	GCC	GCA	CTC	TTC	TGC	CRT	CTG	GTG
V	V	V	V	L	M	S	R	Y	H	R	R	K	A	Q	Q	M	T	K
GTG	GTG	GTG	GTG	CTC	ATG	TCC	CGA	TAC	CAT	CGG	CGC	AAG	GCC	CAG	CAG	ATG	ACC	CAG
Y	E	E	E	L	T	L	T	R	E	N	S	I	R	R	L	H	S	H
TAT	GAG	GAG	GAG	CTG	ACC	CTG	ACC	AGG	GAG	NAC	TCC	ATC	CGG	AGG	CTG	CAT	TCC	CAT
T	D	P	R	S	Q	S	E	E	P	E	G	R	S	Y	S	T	L	T
ACG	GAC	CCC	AGG	AGC	CAG	AGT	GAA	GAG	CCC	GAG	GGC	CGC	AGT	TAC	TCC	ACG	CTG	ACC
V	R	E	I	E	T	Q	T	E	L	L	S	P	G	S	G	R	A	E
GTG	AGG	GAG	ATA	GAA	ACA	CAG	ACT	GAA	CTG	CTG	TCT	CCA	GGC	TCT	GGG	CGG	GCC	GAG
E	E	D	Q	D	E	G	I	K	Q	A	M	N	H	F	V	Q	E	E
GAG	GAA	GAT	CAG	GAT	GAA	GGC	ATC	AAA	CAG	GCC	ATG	AAC	CAT	TTT	GTG	GAG	AAT	GGG
T	L	R	A	K	P	T	G	N	G	I	Y	I	N	G	R	G	H	L
ACC	CTA	CGG	GCC	AAG	CCC	ACG	GGC	AAT	GGC	ATC	TAC	ATC	AAT	GGG	GGG	GGA	CAC	CTG

*

TGA

300
901

Fig. 3H

Fig. 3I

ALT	--							
T364	MPLSLGAEMWGPEAWLILLILLASFTGRCPAGELETSDVVTIVLQDAKLPFCYRGDSGEVQGOVAWARV	10	20	30	40	50	60	
							70	
ALT	--							
T364	DAGEGAQELALLHSKYGLHVSPAYEGRVEQPPPPRNPLDGSVLIRRNAVQADEGEYECCRVSITFPAGSFQAR	80	90	100	110	120	130	140
ALT	--							
T364	LRLRVLYPPLPSLNPGPALEEGQGLTLAASCTAEGSPAPSVTWDTEVKGTSSRSFKHSRSAVTSEFHL	150	160	170	180	190	200	210
ALT	--							
T364	VPSRSWMNGQPLTCVVSHPGLLQDORITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSY	30	40	50	60	70	80	90
ALT	--							
T364	VPSRSWMNGQPLTCVVSHPGLLQDORITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSY	220	230	240	250	260	270	280

Fig. 3J

Fig. 3K

49/67

CTCTAGCTTAAATGAAAGCTGAGTCTGGCAACATCTTTAGGGAGAGGTACAAAGGTTCCTGGACCTTCTC	CTTAATGTTGGAAAGTCTCTTAGTCCATTAGAGAGTGTAGCAGTTGTCCTTGAGACTTCTGGACCTTCTC	55
M M Q E Q O P Q S T E K R G W	AACACAGGGAGCCTGCATA ATG ATG CAA GAG CAG CAA CCT CAA AGT ACA GAG AAA AGA GGC TGG	198
L S L R L W S V A G I S T A L L S A C F	TGG TCC CTG AGA CTC TGG TCT GTG GCT GGG ATT TCC ATT GCA CTC CTC AGT GCT TGC TTC	258
I V S C V V T Y H F T Y G E T G K R L S	ATT GTG AGC TGT GTA ACT TAC CAT TTT ACA TAT GGT GAA ACT GGC AAA AGG CTG TCT	318
E L H S Y H S S L T C F S E G T K V P A	GAA CTA CAC TCA TAT CAT TCA AGT CTC ACC TGC TTC AGT GAA GGG ACA AAG GTG CCA GCC	378
W G C C P A S W K S F G S S C Y F I S S	TGG GGA TGT TGC CCA GCT TCT TGG AAG TCA TTT GGT TCC AGT TGC TAC TTC ATT TCC AGT	438
E E K V W S K S E Q N C V E M G A H L V	GAA GAG AAG GTT TGG TCT AAG AGT GAG CAG AAC TGT GTT GAG ATG GGA GCA CAT TTG GTT	498
V F N T E A E Q N F I V Q Q L N E S F S	GTC ATT GTC CAG CTG AAT GAG TCA ATT GCA TTT TCT GTC ATT GTC CAG CTG AAT GAG TCA ATT	558

Fig. 4A

Y F L G L S D P Q G N N W Q W I D K T 155
 TAT TTT CTG GGG CTT TCA GAC CCA CAA GGT AAT AAT TGG CAA TGG ATT GAT AAG ACA 618

 P Y E K N V R F W H L G E P N H S A E Q 175
 CCT TAT GAG AAA AAT GTC AGA TTT TGG CAC CTA GGT GAG CCC AAT CAT TCT GCA GAG CAA 678

 C A S I V F W K P T G W G W N D V I C E 195
 TGT GCT TCA ATA GTC TTC TGG AAA CCT ACA GGA TGG GGC TGG AAT GAT GTT ATC TGT GAA 738

 T R R N S I C E M N K I Y L * 210
 ACT AGA AGG AAT TCA ATA TGT GAG ATG AAT AAG ATT TAC CTA TGA 783

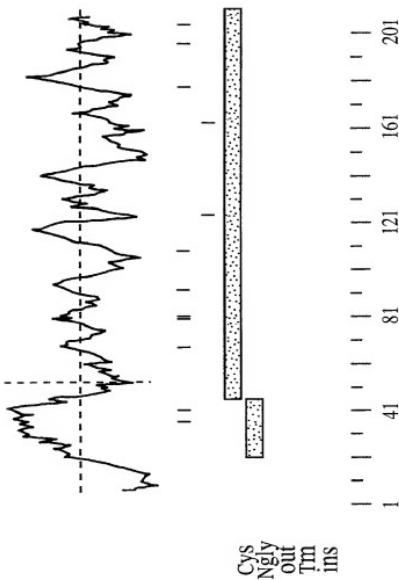
GtGAGAAGCTTAATTGAAAGAAGAAGAATTACTGACGTAAATTTCCTGACGTCTTAAATTCGACCTATCAT 862
 GAAATGATAATTCTTCCTGAAATTACACATAATTCTTTATGTATAGGGTTACAGAAAATGGAAAGATACCTGTTCC 941
 CTTTTAATCAATCTTCCTGTTCTCTTCCATTATGTAGATAATGZACCCTTCTCTCTCTGTTCCATTTTCACTT 1020
 GTTATTCAATTCTTCTCTTCTTCAACACTTCAACAAATATTATATGTTGACTATTTGTTGTTGTTAG 1099
 AAGATTTTAAAGGCAAGTATCTTGTAAATTATGACTTTCCCTCAATTATACCATAAAGAAATCTTGTGGTCAAAGA 1178
 TGGTAGTTGGAACCTAACATTCACTGAAAGGCCGACAAGAGTTGAAAGACATGTTCTAGATGGCTCACTCACATGGCT 1257
 GGCAAACTTGCTGTTGGCTATTAAATGTAACCTGAAATAAATTATTATCTGCAAGTTGGATTGCAATTATATATGT 1336
 TGATTCAATCAAGTTGGCAAGGAGGETTCGATATTCTGTTATATTCTGTTATTTTATTTTCTGAT 1415
 AAATATGTGTTAAATGGCAATGATAATGACAGTTTATTTTATGTTTATTTCTGTTATTTCTGTTATTTCTGTTAG 1494
 AAGCATTCTTGTGTTACCCAAATCTAACCTPATTCCTGAAAAATATGATGGTTAGAAAGTTGAGATAACTAGGCCTGTA 1573
 ATCCATCATTTAAATGGCAATTCAACAAATTCTGATTTTACACATTAAACAAATGACATTAAACAAATGACATT 1652
 TACCAAAATGGTCAATTAACTGATTCACATACCTTAAAGGATTCTGCAATTACACTTAAACAAATGACATT 1731

Fig. 4B

GCAATTAAACCTTATGGGGCATGACTATATGCCAACAGTTGATGATAATGATAAAATTATGTTTTCCTTTCCA 1810
 TTGCACTGAAAATCCATATAAAGAAGAACATCCCATCATTCCAATTTGCCCCATATTGATTGATACTCGAAGAATC 1889
 TGGCACTGAGGCCCATAAAGGGATAAGCAATTGGGAAGGGATTGGGAAGTTGGTAGTGTAGATGAAACATCTCACCTGG 1968
 ACTCATGAGCAACTGAAACTGAAATAGTTGTAACUTGATGATACTGGAAATTTAAACATTTTCCCTTGAAATTAGAAATT 2047
 GGCAAAACAAATTCTTAATTAAATTAGCAAATATTGGATAATTAAAGCTTCTTAAAGAGATACTCTTATATTAA 2126
 AGCCATGATGAGGTATAACAATGTTATAAATTACTTGTACATGGCAATTAAATTATTTTATCAATGTCGAGTCACT 2205
 TTCTTTAAATTAGTAAATGGCTTAAATTCTCTGTATAATTAAATTAGATACTGAACTTCAATTATGTTAG 2284
 TGCTGTAAAAATTCTTCTTCCATCTTCAATTTCACCTTATTCACATGCTCTTAATAAGTGTATATAAGT 2363
 AAATTCTAAAAAAATCCAAATGGCAATCACCCTTAACTTAAATTAACTTCAATTGTGACZATTGACATA 2442
 TATATGGTTCTAACTCTCATCTTACTAGGGTGTTCATTCTCTGCTCCTAAATAATTTTTAAAGCTTATAAC 2521
 ACAACTTTTAAATTAGAAAAGTTTACATAAACAGGATAACTTCTTCAAGAACCCAATAAGAACCAAACAGACTA 2600
 ACAAAATGTGTAACAGAAACTAAACATTCATTATGACCTTCTTAAATCAACATTCATTATCTACAATGTTTAAACAGGG 2679
 AAAAACTCCATGGTTAACGGCATGTCAATTGAAATAAGCTGCAATTAGCTTCTTAACTAATTTGCTCTCAAGAAA 2758
 ATGAAATCATTAAGCAGTAATTAGGGATTCACAAATTAAACATTCACTGTAATTGTTAAATTATGTTCTTAATAATT 2837
 TTAAAATTATGAAAGTCGAGTTCAAAAGTGAATTCTCCCAAAAGGTGCCAAACTTAAGCTAGACCTTCAGTGT 2916
 AACTTTGCCCTAAAGTTAGACATATTCTGAGAACTATAATGTCACATGATTCTGAGCTTATGCTCTGTAAATA 2995
 ACAAAAGATTCAACATGAAACCTTGTAAACAAATTCTCCATGTTCTACATATAACCTAAAGTATAATAAA 3074
 TAATAAAACATGCAAGGCTTTAAAAAAAAAAAAAAAA 3114

Fig. 4C

FIG. 4D



GAACTCCCCGGTGTGACCCCCGGTCCCGATTGGCCGCTCTGGCATTTAAGTCAAGTGTGTGGAAAGTGTGATTCT 79
 GAACTCTGGCTCTTTGACAGAACGGTCCCTGAGTCGTATTTGGAGACAGATGCAGAACCCCTGACCTCTGA 158

 M V Q E R Q S Q G K G V C W T L 16
 ACATAACCTCACACA ATG GTG CAG GAA AGA CAA TCC CAA GGG AAG GGA GTC TGC TGG ACC CTG 221

 R L W S A A V I S M L L S T C F I A S 36
 AGA CTC TGG TCA GCT GCT GTG ATT TCC ATG TTA CTC TTG AGT ACC TGT TTC ATT GCG AGC 281

 C V T Y Q F I M D Q P S R R L Y E L H 56
 TGT GTG GTG ACT TAC CAA TTT ATT ATG GAC CAG CCC AGT AGA CTA TAT GAA CTT CAC 341

 T Y H S S L T C F S E G T M V S E K M W 76
 ACA TAC CAT TCC AGT CTC ACC TGC TTC AGT GAA GGG ACT ATG GTG TCA GAA AAA ATG TGG 401

 G C C P N H W K S F G S S C Y L I S T K 96
 GGA TGC TGC CCA AAT CAC TGG AAG TCA TTT GGC TCC AGC TAC CTC ATT TCT ACC AAG 461

 E N F W S T S E Q N C V Q M G A H L V V 116
 GAG AAC TTC TGG AGC ACC AGT GAG CAG AAC TGT GTT CAG ATG GGG GCT CAT CTG GTG GTG 521

 I N T E A E Q N F I T Q Q L N E S L S Y 136
 ATC AAT ACT GAA GCG GAG CAG ACC ATC ACC CAG CAG CTG AAT GAG TCA CTT TCT TAC 581

Fig. 4E

የጊዜ የጥቃት ተስፋ ተስፋ ስርዓት የጥቃት

F	L	G	L	S	D	P	K	V	M	A	N	G	N	G	S	M	I	L	L	156
TTC	CTG	GGT	CTT	TCG	GAT	CCC	AAG	GTA	ATG	GCA	AAT	GGC	AAT	GGA	TCG	ATG	ATA	CTC	CTT	641
S	V	K	M	S	G	S	G	T	P	M	N	P	I	F	Q	K	S	G	V	176
TCA	GTC	AAA	ATG	TCA	GGT	TCT	GGC	ACC	CCC	ATG	AAC	CCA	ATC	TTC	CAG	AAG	AGC	GGT	GTG	701
F	Q	*																		179
TTT	CAA	TAG																		710

TTTACTGGAAATCCTTCGAAATGGGGCTGGGAATGATGTTTTCTGGATAGTAAACACAATTCAATAATGTGAAATGAAANA
AGATTACCTATGAATGCCCTGTTATCTTAATA

Fig. 4F

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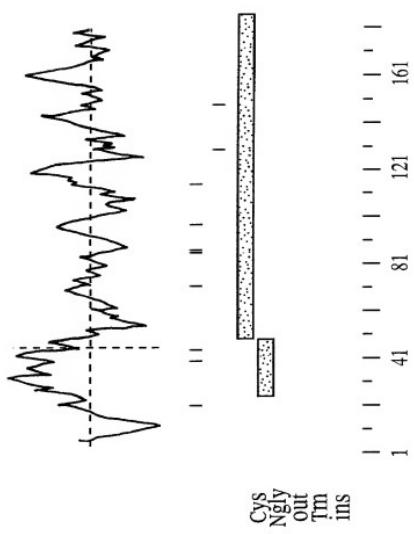


FIG. 46

human	MQEQQPQSTKEKGWLSSLRLWVAGISIALLSACFIVSCUVTYHFTYGETGKRLSELHSYHSSLTCFSEG ::: ::::: ::: :::::	10	20	30	40	50	60	70
murine	MVQEROSQGKVQ-W-TLRLWSAAVISMILLSTCFIASCVVTYQIMDQPSRRLXYELHTYHSSLTCFSEG ::: ::::: ::: :::::	10	20	30	40	50	60	
human	TKVPA--WGCCCASWKSFGGSSCYFISSEERVWSKSEQNCYEMGAHLVVVENTEAONFTVQQLNESFSYFL ::: ::::: ::: :::::	80	90	100	110	120	130	
murine	TMSERMWMGCPNHWKSFGGSSCYLISTKENFWSTSEQNVCQMGAHLLVINTEEAQNFITQQLNESFSYFL ::: ::::: ::: :::::	70	80	90	100	110	120	130
human	GLSDPQGNNNWWQWIDKTPYEKVNVRFHILGEPNHSAEQCASIVFWKPTGWGNNDVICTRRNICMENKIV ::: ::::: ::: :::::	140	150	160	170	180	190	200
murine	GLSDPKVMAN-----GNGSMILLSV--KMSGSG-----TPMNP1FQKSGVF ::: ::::: ::: :::::	140	150	160	170	180	190	170

Fig. 4H

human L

nurine Q

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human	ATGATCAGGAGCAGCAACCTCAAAGTACAGAGAAAAGGGCTGGTTGAGACTCTGGTCTGTGG	10	20	30	40	50	60	70
murine	ATGGTGCAGAAAGACAATCCCA-----AGGAAGGAGTCGCTGGACCCGTAGACTCTGGTCA	10	20	30	40	50	60	
human	CTGGGATTCCATTGCACTCTCAGTGCTCATGTGAGCTGTAGTAACCTTACATTTACATA	80	90	100	110	120	130	140
murine	CTGTGATTCCATTGTTACTCTTGAGTACTGTGTTCATGCGAGCTGTGGTGAACCTAACATTAT	70	80	90	100	110	120	130
human	TGGTGAAGACTGGCAAAGGCTGTGAACCTACATCATTCAGTCACCTCAAGTCTCAC	150	160	170	180	190	200	210
murine	GGACCAGGCCAGTAGAAGACTATATGAACATTACACATACCCAGTCTCAC	140	150	160	170	180	190	200
human	ACAAAGGTGCAGCC-----TGGGGATGTTGCCAGCTTGGAGTCATTGGTTCCAGTGTACT	220	230	240	250	260	270	
murine	ACTATGGGTGTCAGAAAAAAATGGGGGATGCTGCCAAATCACTGGAGTCATTGGCTCCAGGTAC	210	220	230	240	250	260	270

Fig. 4I

TGTGTTGCTTGGATTTGGGAGGAA

human	TCATTTCCAGTGAGAGAAGGTTGGTCTTAAGGTGAGCAGAACCTGTTGAGATGGAGCACATTGGT	280	290	300	310	320	330	340
murine	TCATTTCTACCAAGGGAGAACCTCTGGACACCAGTGAGAACCTGTTGAGACTGTGTTGAGATGGGGCTATATCTGGT	280	290	300	310	320	330	340
human	TGTGTTCAACACAGAAAGCAGCAGGAATTTCATGGTCAGCAGCTGATGAGTCATTTCCTTATTTCTG	350	360	370	380	390	400	410
murine	GGTGTACAATACTGAAGGGAGCAGGAATTTCATACCCAGCAGCTGAAATGAGTCACTTTCTTACTTCCCTG	350	360	370	380	390	400	410
human	GGGCCTTCAGACCCACAAGGTAATAATTGGCAATTGGATTGATAGACACCTTATGAGAAAATGTCA	420	430	440	450	460	470	480
murine	GGTCUTTCGGATCC-CAAGGTTAATGGCAAATGGGAATGGATCGATACTCCTTCAGTCAAAATGTCA	420	430	440	450	460	470	480
human	GATTTGGCACCTAGGTGAGGCCAATCATTTCTGAGAGCAATGTGCTTCAATAGTCTTCTGGAAACCTAC	490	500	510	520	530	540	550
murine	GGTCTGGCACCCCATGAACCAATCTCCAGAAGAGCGGTGTCAA-----	490	500	510	520	530	540	550

Fig. 4J

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human AGGATGGGCTGGAAATGATGTTATCTGTAACTAGAAGGAATTCAATATGTGAGATGAATAAGATTAC
murine -----

human CTA
murine ----

Fig. 4K

DECTIN-1 TTS952650

mT405	MVQERQSQQGKGVCVTLRLWSAAVISMILLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFCSEGTM	10	20	30	40	50	60	70
Dectin	MVQERQSQQGKGVCVTLRLWSAAVISMILLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFCSEGTM	10	20	30	40	50	60	70
mT405	VSEKMWGCCPNHWKSFSSCYLISTKENFWSTSEQNCVQMGAAHLVVVINTEAEQNFTIQNLNESLSYFLGL	80	90	100	110	120	130	140
Dectin	VSEKMWGCCPNHWKSFSSCYLISTKENFWSTSEQNCVQMGAAHLVVVINTEAEQNFTIQNLNESLSYFLGL	80	90	100	110	120	130	140
mT405	SDBPKVMAN---GNGSMILLSVKMSGSGTPMNP-----IF-----QKSGVFQ	150	160	170				
Dectin	SDBQGNGKRWOWIDDTFSQNRFWHPHEPNLPEERCVSIVYWNPSPKGWNNDVFCDSKHNSICEMRKIYL	150	160	170	180	190	200	

Fig. 4L

ht405 MNQQPQPOSTEKRGWILSLRLWSVAGISIALSACFIVSCVVITYHFTYGETGKRSELHSYHSSLTCFSEG ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: Dectin MVQEROSQGKGV-C-W-TIRIWSAAVISMLLSTCFIASCVVITYQFDQPSRRIYELHTYISSLTFCFSEG 10 20 30 40 50 60 70	ht405 TKVPA--WGCCPASWKSGSCYFISSEEKYWSKSEQNCEVNGAHLVVNTEAEQNFTYQQINESFSYFL ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: Dectin TMVSERMWGCPPNHWSFGSCYLISTKENFWSTSEQNCFVQMGAHLLVVNTEAEQNFTQQLNESLSYFL 80 90 100 110 120 130 140	ht405 GLSDPQGNNNWWQWIDKTPYEKNVRFWHIGEPNHSAEQCASIVFWKPTGWNNDVICETRNSLCEMNKIYL ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: Dectin GLSDFQGNKGKWQWIDDIPFSQNVRFWHPHEPNLPEERCVSIVZMNSKWNDFCDSKINSICEMKKIYL 150 160 170 180 190 200
--	--	---

Fig. 4M

5' UGGTTGTTTSSSSGCGG

CGACCCCGGG TCCGCTGACT TCTGGGTTG CAGCATGGC CCGCTCTGG GCATTAACT	60
CAAGTGTG TGGAAGTTGA TTCTGAACCT TGGCTCTTT GACAGAAGCC AGGTCCCTGA	120
GTCGTATTTT GGAGACAGAT GCAAGAAACC CCTGACCTTC TGAACATACA CCTCAACA	178
ATG GTG CAG GAA AGA CAA TCC CAA GGG AAG GGA GTC TGC TGG ACC CTG	226
Met Val Glu Arg Gln Ser Gln Gly Lys Gly Val Cys Trp Thr Leu	15
5	
AGA CTC TGG TCA GCT GCT GTG ATT TCC ATG TTA CTC TTG AGT ACC TGT	274
Arg Leu Trp Ser Ala Ala Val Ile Ser Met Leu Leu Ser Thr Cys	30
20	
25	
TTC ATT GCG AGC TGT GTG GTG ACT TAC CAA TTT ATT ATG GAC CAG CCC	322
Phe Ile Ala Ser Cys Val Val Thr Tyr Gln Phe Ile Met Asp Gln Pro	45
35	
40	
AGT AGA AGA CTA TAT GAA CTC CAC ACA TAC CAT TCC AGT CTC ACC TGC	370
Ser Arg Arg Leu Tyr Glu Leu His Thr Tyr His Ser Ser Leu Thr Cys	55
50	
TTC AGT GAA GGG ACT ATG GTG TCA GAA AAA ATG TGG GGA TGC TGC CCA	418
Phe Ser Glu Gly Thr Met Val Ser Glu Lys Met Trp Gly Cys Cys Pro	80
65	
70	
75	

Fig. 4N

AAT CAC TGG AAG TCA TTT GGC TCC AGC TGC TAC CTC ATT TCT ACC AAG	466
Asn His Trp Lys Ser Phe Gly Ser Ser Cys Tyr Leu Ile Ser Thr Lys	
85	95
GAG AAC TTC TGG AGC ACC AGT GAG CAG AAC TGT GTT CAG ATG GGG GCT	514
Glu Asn Phe Trp Ser Thr Ser Glu Gln Asn Cys Val Gln Met Gly Ala	
100	110
CAT CTG GTG ATC AAT ACT GAA GCG GAG CAG AAT TTC ATC ACC CAG	562
His Leu Val Val Ile Asn Thr Glu Ala Glu Gln Asn Phe Ile Thr Gln	
115	125
CAG CTG AAT GAG TCA CTT TCT TAC TTC CTG GGT CCT TCG GAT CCA CAA	610
Gln Leu Asn Glu Ser Leu Ser Tyr Phe Leu Gly Leu Ser Asp Pro Gln	
130	140
GGT AAT GGC AAA TGG CAA TGG ATC GAT GAT ACT CCT TTC AGT CAA AAT	658
Gly Asn Gly Lys Trp Gln Trp Ile Asp Asp Thr Pro Phe Ser Gln Asn	
145	155
GTC AGG TTC TGG CAC CCC CAT GAA CCC AAT CTT CCA GAA GAG CGG TGT	706
Val Arg Phe Trp His Pro His Glu Pro Asn Leu Pro Glu Glu Arg Cys	
165	170
	175

Fig. 4O

Phe Cys Asp Ser Lys His Asn Ser Ile Cys Glu Met Lys Ile Tyr

GTT TCA ATA GTT TAC TGG AAT CCT TCG AAA TGG GGC TGG AAT GAT GTT	754
Val Ser Ile Val Tyr Trp Asn Pro Ser Lys Trp Gly Trp Asn Asp Val	
180	185
TTC TGT GAT AGT AAA CAC AAT TCA ATA TGT GAA ATG AAG ATT TAC	802
Phe Cys Asp Ser Lys His Asn Ser Ile Cys Glu Met Lys Ile Tyr	
195	200
205	
CTA TGA GTGCCGTATA TTCCATTATA TCTTTAAAGT TCAGACCTAC CAAGAACCA	858
Leu *	
TAACTTCTG GCCTGTACAT CTGACAGAGG CCGTTCTTT CCTAGCCACT ATTCTTTACT	918
CAAACAGAT GAGCCCTTC TCCTCTGTAT GGTTAGAGTT TTGTCAACTT GACACAACT	978
AGAGTCACCT GGGGAGTAGG ATCTCAGCT AAGGAATTGC CTCTGTCAAGC TTGACAGTC	1038
AGCATGTCTG GGGGCATTCTT CTTGATTAAAT GATTGTTGTA AGAGGGTCCA GGTGGTAAGC	1098
AAAGGTGTTA AACCCATGAA GAGCAAGCCA GGGGAGATCA TCCATCCATC TCTGCCCTCA	1158
GGTTTCTGCC CCAGGGTCITT GCCCTGGTTT CTTTCTATGA ACTGCTGTTA CTTGAAAGTA	1218
TAAGATGAAT AAACAATTTC ATCCAAAAAA AAAA	1252

Fig. 4P

Fig. 5A

GTGAAACCTGTCTACTAAACATACAAAATTAGTGGGGTGTGGCATGGCCTGTAATTCCAGCT
 1043
 1113
 1183
 1202
 ACTCAGGGGTGAGCAGGAATCCTGAACCCAGGGCAGAGATTACAGTGAGCCGAGATCATGCC
 CCTTGCACTTAGCTGGGTGACAGCGAGACTCTGTCTAAAAA
 AAAAAAAAGGGGGCGC

Fig. 5B

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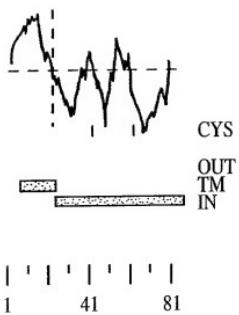


FIG. 5C